












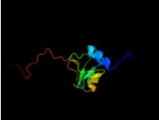











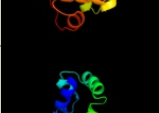







#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1sfeA_	 Alignment		100.0	99	PDB header: dna-binding protein Chain: A: PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli
2	c1wrjA_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
3	c1zgwA_	 Alignment		100.0	98	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polypeptide; PDBTitle: nmr structure of e. coli ada protein in complex with dna
4	c1t39A_	 Alignment		100.0	34	PDB header: transferase/dna Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
5	c1mgtA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: protein (o6-methylguanine-dna methyltransferase); PDBTitle: crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
6	c2g7hA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: structure of an o6-methylguanine dna methyltransferase from2 methanococcus jannaschii (mj1529)
7	d1eyfa_	 Alignment		100.0	97	Fold: Ada DNA repair protein, N-terminal domain (N-Ada 10) Superfamily: Ada DNA repair protein, N-terminal domain (N-Ada 10) Family: Ada DNA repair protein, N-terminal domain (N-Ada 10)
8	d1sfeal	 Alignment		100.0	98	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
9	d1qntal	 Alignment		100.0	44	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
10	c3gx4X_	 Alignment		100.0	28	PDB header: dna binding protein/dna Chain: X: PDB Molecule: alkyltransferase-like protein 1; PDBTitle: crystal structure analysis of s. pombe atl in complex with dna
11	c2kimA_	 Alignment		99.9	24	PDB header: transferase Chain: A: PDB Molecule: o6-methylguanine-dna methyltransferase; PDBTitle: 1.7-mm microcryoprobe solution nmr structure of an o6-2 methylguanine dna methyltransferase family protein from3 vibrio parahaemolyticus. northeast structural genomics4 consortium target vpr247.

12	d1mgta1	Alignment		99.9	37	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
13	c3gbgA	Alignment		99.9	11	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of tcp from vibrio cholerae o395
14	c1d5yD	Alignment		99.9	23	PDB header: transcription/dna Chain: D: PDB Molecule: rob transcription factor; PDBTitle: crystal structure of the e. coli rob transcription factor2 in complex with dna
15	c2k9sA	Alignment		99.9	24	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
16	c3oioA	Alignment		99.9	27	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (arac-type dna-binding domain- PDBTitle: crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
17	c3oouA	Alignment		99.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unknown function from listeria innocua
18	c1bl0A	Alignment		99.9	20	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
19	c3mn2B	Alignment		99.8	19	PDB header: transcription regulator Chain: B: PDB Molecule: probable arac family transcriptional regulator; PDBTitle: the crystal structure of a probable arac family transcriptional2 regulator from rhodospseudomonas palustris cga009
20	c3mklB	Alignment		99.8	13	PDB header: transcription regulator Chain: B: PDB Molecule: hth-type transcriptional regulator gadx; PDBTitle: crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
21	d1sfea2	Alignment	not modelled	99.7	100	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
22	c3lsgD	Alignment	not modelled	99.7	17	PDB header: transcription regulator Chain: D: PDB Molecule: two-component response regulator yesn; PDBTitle: the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
23	d1d5ya2	Alignment	not modelled	99.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
24	d1bl0a2	Alignment	not modelled	99.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
25	d1d5ya1	Alignment	not modelled	98.5	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
26	d1bl0a1	Alignment	not modelled	98.5	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
27	d1qnta2	Alignment	not modelled	97.5	22	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
28	d1biaa1	Alignment	not modelled	90.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
29	d1j5ya1	Alignment	not modelled	90.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

					Family: Biotin repressor-like
30	d2hsga1	Alignment	not modelled	90.5	20 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
31	c3eusB	Alignment	not modelled	89.8	9 PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroiyi
32	d1mkma1	Alignment	not modelled	89.5	15 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator ICLR, N-terminal domain
33	d1qpza1	Alignment	not modelled	88.9	15 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
34	d2cg4a1	Alignment	not modelled	88.2	20 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
35	d1efaa1	Alignment	not modelled	87.8	24 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
36	d2icta1	Alignment	not modelled	87.7	27 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
37	c1bdhA	Alignment	not modelled	86.4	12 PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
38	c1mkmA	Alignment	not modelled	86.4	15 PDB header: transcription Chain: A: PDB Molecule: iclR transcriptional regulator; PDBTitle: crystal structure of the thermotoga maritima iclR
39	d1lcda	Alignment	not modelled	86.4	24 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
40	d2cyva1	Alignment	not modelled	86.3	9 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
41	d1ilga1	Alignment	not modelled	86.1	17 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
42	c2vzbA	Alignment	not modelled	86.0	20 PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
43	c3h5tA	Alignment	not modelled	85.9	22 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
44	c2bnoA	Alignment	not modelled	85.8	10 PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
45	d2cfxa1	Alignment	not modelled	85.8	11 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
46	c2l4aA	Alignment	not modelled	85.6	14 PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
47	d2bjca1	Alignment	not modelled	85.4	17 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
48	d1xd7a	Alignment	not modelled	85.1	24 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
49	c2g7uB	Alignment	not modelled	84.9	18 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
50	c2xroE	Alignment	not modelled	84.8	18 PDB header: dna-binding protein/dna Chain: E: PDB Molecule: hth-type transcriptional regulator ttgV; PDBTitle: crystal structure of ttgV in complex with its dna operator
51	c3clcC	Alignment	not modelled	84.8	17 PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp13961 tetramer in complex with its natural 35 base-pair operator
52	d1y7ya1	Alignment	not modelled	84.5	15 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
53	c2e1cA	Alignment	not modelled	84.3	9 PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
54	d1sq8a	Alignment	not modelled	84.2	17 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
55	d1sgma1	Alignment	not modelled	84.1	13 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
					Fold: lambda repressor-like DNA-binding domains

56	d2croa_	Alignment	not modelled	83.4	13	Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
57	c2cg4B_	Alignment	not modelled	83.3	20	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
58	c1ilgA_	Alignment	not modelled	83.3	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
59	c1zvva_	Alignment	not modelled	82.9	19	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
60	d2b5aa1	Alignment	not modelled	82.9	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
61	c2ia2D_	Alignment	not modelled	82.8	15	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
62	c1y9gA_	Alignment	not modelled	82.2	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
63	c2e7xA_	Alignment	not modelled	81.9	14	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
64	c2lcvA_	Alignment	not modelled	81.3	14	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
65	c2cfxD_	Alignment	not modelled	81.3	11	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpC; PDBTitle: structure of b.subtilis lrpC
66	c2dbbA_	Alignment	not modelled	81.3	17	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
67	c3i4pA_	Alignment	not modelled	81.2	20	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
68	d1lilb_	Alignment	not modelled	81.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
69	c1sgmA_	Alignment	not modelled	81.0	13	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator yxaf; PDBTitle: crystal structure of hypothetical protein yxaf
70	c3r4kD_	Alignment	not modelled	80.8	13	PDB header: dna binding protein Chain: D: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
71	d1y9qa1	Alignment	not modelled	80.7	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
72	c3f6wE_	Alignment	not modelled	80.6	11	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
73	c3f52A_	Alignment	not modelled	80.3	21	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
74	c2ia0A_	Alignment	not modelled	80.2	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
75	d1rioa_	Alignment	not modelled	80.2	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
76	c2p6tH_	Alignment	not modelled	79.9	26	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
77	c2dg7A_	Alignment	not modelled	79.7	16	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
78	c2wgbB_	Alignment	not modelled	79.7	16	PDB header: transcription Chain: B: PDB Molecule: tetr family transcriptional repressor lfrr; PDBTitle: crystal structure of the tetr-like transcriptional2 regulator lfrr from mycobacterium smegmatis
79	d1lmb3_	Alignment	not modelled	79.6	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
80	c2l8nA_	Alignment	not modelled	79.4	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
81	d2i10a1	Alignment	not modelled	79.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like

					Family: Tetracyclin repressor-like, N-terminal domain
82	d1uxca_	Alignment	not modelled	79.2	7 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
83	c3mkyp_	Alignment	not modelled	78.9	19 PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
84	c3iuvA_	Alignment	not modelled	78.8	17 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized tetr family protein; PDBTitle: the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3
85	c3bs3A_	Alignment	not modelled	78.5	15 PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
86	c3op9A_	Alignment	not modelled	78.5	8 PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
87	d1z05a1	Alignment	not modelled	78.5	14 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
88	d1hlva1	Alignment	not modelled	78.3	14 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
89	d2fq4a1	Alignment	not modelled	78.3	16 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
90	c2oerA_	Alignment	not modelled	77.9	16 PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: probable transcriptional regulator from pseudomonas2 aeruginosa
91	d1t56a1	Alignment	not modelled	77.8	24 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
92	d1jt6a1	Alignment	not modelled	77.7	15 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
93	d2g7ga1	Alignment	not modelled	77.6	15 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
94	c2x4hA_	Alignment	not modelled	77.6	7 PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
95	c2ebyA_	Alignment	not modelled	77.3	8 PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
96	d2jn6a1	Alignment	not modelled	77.3	17 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
97	c3kjd_	Alignment	not modelled	76.9	18 PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
98	c3omtA_	Alignment	not modelled	76.6	9 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
99	d2g3ba1	Alignment	not modelled	76.5	20 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
100	d1v7ba1	Alignment	not modelled	76.4	14 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
101	d1adra_	Alignment	not modelled	76.1	14 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
102	d1vi0a1	Alignment	not modelled	75.8	13 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
103	c2i10A_	Alignment	not modelled	75.7	15 PDB header: transcription Chain: A: PDB Molecule: putative tetr transcriptional regulator; PDBTitle: putative tetr transcriptional regulator from rhodococcus sp. rha1
104	c2guhA_	Alignment	not modelled	75.7	21 PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
105	d2gena1	Alignment	not modelled	75.7	18 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
106	c1jumB_	Alignment	not modelled	75.6	17 PDB header: transcription Chain: B: PDB Molecule: hypothetical transcriptional regulator in qaca PDBTitle: crystal structure of the multidrug binding transcriptional2 repressor qacr bound to the natural drug berberine
107	d1umqa_	Alignment	not modelled	75.5	10 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like

108	c1umqA_	 Alignment	not modelled	75.5	10	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
109	c3hosA_	 Alignment	not modelled	75.5	17	PDB header: transferase, dna binding protein/dna Chain: A: PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex with mg
110	c2g7gA_	 Alignment	not modelled	75.4	13	PDB header: transcription Chain: A: PDB Molecule: rha04620, putative transcriptional regulator; PDBTitle: the crystal structure of the putative transcriptional regulator2 rha04620 from rhodococcus sp. rha1
111	d1r69a_	 Alignment	not modelled	75.3	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
112	c2f07A_	 Alignment	not modelled	75.2	4	PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis
113	d2fx0a1	 Alignment	not modelled	75.2	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
114	c3ivpD_	 Alignment	not modelled	75.1	9	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
115	c3ppbB_	 Alignment	not modelled	74.9	12	PDB header: transcription regulator Chain: B: PDB Molecule: putative tetr family transcription regulator; PDBTitle: crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
116	d2o7ta1	 Alignment	not modelled	74.6	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
117	c3mkzU_	 Alignment	not modelled	74.6	19	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
118	c1hlvA_	 Alignment	not modelled	74.5	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
119	d2vkea1	 Alignment	not modelled	74.5	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
120	c3b6aC_	 Alignment	not modelled	74.4	17	PDB header: transcription Chain: C: PDB Molecule: actr protein; PDBTitle: crystal structure of the streptomyces coelicolor tetr2 family protein actr in complex with actinorhodin